

Amendments to the Specification

At page 5, in the first paragraph beginning at line 2:

These techniques presently suffer from several disadvantages. Perhaps most important is their limited quantitative reproducibility, which ~~leads to a significance~~ leads to a significant incidence of false positive signals, as much as 80% in the case of differential display. (As described regarding differential display in *Trends Genet.* 11: 242 *et seq.* (1995), *Nuc. Acids Res.* 22: 5763, *et seq.* (1994) and *FEBS Lett.* 351: 231 *et seq.* (1994), among others). Furthermore, the hybridization techniques generally are useful only to analyze expression of genes whose sequences already are known hybridization chip technology has not yet produced arbitrary sequence arrays that could assay the expression complement even of relatively small genomes. Differential display and oligo-chip techniques furthermore suffer from irreproducibility caused by unpredictable hybridization of random short sequence probe sets to high complexity targets under low stringency conditions.

On page 5, in the 2nd paragraph beginning at line 20:

A reproducible technique for profiling gene expression with great quantitative accuracy has been described; more recently. In its most common format, this technique quantitatively determines mRNA abundance in samples by measuring the amounts of 3'-end fragments of cDNAs generated by specific primers and specific cleavage reactions. The technique is described in detail in pending PCT patent application number PCT US96 12468, published as WIPO publication W097 05286, dated 13 February 1997, the disclosure of which is incorporated herein, in its entirety.

On page 31, in the 2nd paragraph beginning at line 29:

Similarly, the n-dimensional display space of molecular topographies of the present invention can be defined by a variety of characteristics indicated along an axis. Thus, for instance, an a three dimensional display space of the present invention may be defined by three ~~axis~~ axes, one of which relates to such identifying sequences in DNA or mRNA of a sample as repeat sequences, motifs related to cis-acting or trans-acting control elements, specific mutations of mitochondrial or genomic DNA, characteristic motifs, such as motifs associated

with particular types and functions of proteins, sequences defined by primers or by specific cleavage, and other such structural or functional sequence-specific DNA or mRNA characteristics characteristics